



SEQUENCE LISTING

<110> Schrier, Peter I.  
Aarnoudse, Corlien A.  
Heider, Karl-Heinz  
Wiener, Christoph Klade

<120> Camel, an Alternative Translation Product of the Tumor Antigen Lage-1

<130> 0652.2200000

<140> 09/807,512

<141> 2002-04-08

<150> PCT/EP99/07832

<151> 1999-10-15

<150> EP 98119583.7

<151> 1998-10-16

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<170> PatentIn Ver. 2.1

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Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala  
15 20 25

GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG CCT CGG GGC CGA GAG GAG 144  
Glu Val Pro Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu  
30 35 40 45

GCG CCC CGC GGG GTC CGC ATG GCG GTG CCG CTT CTG CGC AGG ATG GAA 192  
Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu  
50 55 60

GGT GCC CCT GCG GGG CCA GGA GGC CGG ACA GCC GCC TGC TTC AGT TGC 240  
Gly Ala Pro Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys  
65 70 75

ACA TCA CGA TGC CTT TCT CGT CGC CCA TGG AAG CGG AGC TGG TCC GCA 288  
Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala  
80 85 90

GGA TCC TGT CCC GGG ATG CCG CAC CTC TCC CCC GAC CAG GGG CGG TTC 336  
Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe  
95 100 105

TGA AGGACTTCAC CGTGTCCGGC AACCTACTGT TTATCCGACT GACTGCTGCA 389

GACCACCGCC AACTGCAGCT CTCCATCAGC TCCTGTCTCC AGCAGCTTTC CCTGTTGATG 449

TGGATCACGC AGTGCTTTCT GCCCGTGTTT TTGGCTCAGG CTCCCTCAGG GCAGAGGCGC 509

TAAGCCAGC CTGGCGCCCC TTCCTAGGTC ATGCCTCCTC CCCTAGGGAA TGGTCCCAGC 569

ACGAGTGGCC AGTTCATTGT GGGGGCCTGA TTGTTTGTCTG CTGGAGGAGG ACGGCTTACA 629

TGTTTGTTC TGTAGAAAAT AAAGCTGAGC TACGAAAAAA AAAAAAAAAA 679

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Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
20 25 30

Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
35 40 45

Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro  
50 55 60

Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg  
65 70 75 80

Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys  
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Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe  
100 105

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Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
5 10 15	
CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	152
Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
20 25 30	
CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGG	200
Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
35 40 45	
GCA GCA AGG GCC TCG GGG CCG AGA GGA GGC GCC CCG CGG GGT CCG CAT	248
Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
50 55 60 65	
GGC GGT GCC GCT TCT GCG CAG GAT GGA AGG TGC CCC TGC GGG GCC AGG	296
Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	
70 75 80	
AGG CCG GAC AGC CGC CTG CTT CAG TTG CAC ATC ACG ATG CCT TTC TCG	344
Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	
85 90 95	
TCG CCC ATG GAA GCG GAG CTG GTC CGC AGG ATC CTG TCC CGG GAT GCC	392
Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	
100 105 110	
GCA CCT CTC CCC CGA CCA GGG GCG GTT CTG AAG GAC TTC ACC GTG TCC	440
Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	
115 120 125	
GGC AAC CTA CTG TTT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG	488
Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu	
130 135 140 145	
CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG	536

Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp	
150 155 160	
ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG GCT CCC TCA GGG	584
Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly	
165 170 175	
CAG AGG CGC TAA GCCCAGCCTG GCGCCCCTTC CTAGGTCATG CCTCCTCCCC	636
Gln Arg Arg	
180	
TAGGGAATGG TCCCAGCACG AGTGGCCAGT TCATTGTGGG GGCCTGATTG TTTGTCGCTG	696
GAGGAGGACG GCTTACATGT TTGTTTCTGT AGAAAATAAA GCTGAGCTAC GAAAAAAAAA	756
AAAAAAAAA A	767

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35 40 45	
Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro	
50 55 60	
His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala	
65 70 75 80	
Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe	
85 90 95	
Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp	
100 105 110	
Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val	
115 120 125	
Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln	
130 135 140	
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met	
145 150 155 160	
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Gly Gln Arg Arg	
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Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
5 10 15	
CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	154
Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
20 25 30	
CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGC	202
Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
35 40 45	
GCA GCA AGG GCC TCG GGG CCG AGA GGA GGC GCC CCG CGG GGT CCG CAT	250
Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
50 55 60 65	
GGC GGT GCC GCT TCT GCG CAG GAT GGA AGG TGC CCC TGC GGG GCC AGG	298
Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	
70 75 80	
AGG CCG GAC AGC CGC CTG CTT CAG TTG CAC ATC ACG ATG CCT TTC TCG	346
Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	
85 90 95	
TCG CCC ATG GAA GCG GAG CTG GTC CGC AGG ATC CTG TCC CGG GAT GCC	394
Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	
100 105 110	
GCA CCT CTC CCC CGA CCA GGG GCG GTT CTG AAG GAC TTC ACC GTG TCC	442
Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	
115 120 125	
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Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly Ala	

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GGG CGG ATG AGG GTG GTG GGT TGG GGG CTG GGA TCC GCC TCC CCG GAG				538
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Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu	165	170	175	
CAG AGA CCT GGT ACA CCA GGC CCG CCG CCA CCC GAG GGA GCC CAG GGA				634
Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Glu Gly Ala Gln Gly	180	185	190	
GAT GGG TGC AGA GGT GTC GCC TTT AAT GTG ATG TTC TCT GCC CCT CAC				682
Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His	195	200	205	
ATT TAG CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC ATCAGCTCCT				738
Ile				
210				
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CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCCTTCC TAGGTCATGC				858
CTCCTCCCCCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG GCCTGATTGT				918
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Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro	50	55	60	
His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala	65	70	75	80
Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe	85	90	95	
Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp				

100	105	110
Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val		
115	120	125
Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly		
130	135	140
Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro		
145	150	155
Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser		
165	170	175
Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln		
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195	200	205
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Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
5 10 15	
CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	152
Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
20 25 30	
CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGC	200
Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
35 40 45	

GCA GCA AGG GCC TCG GGG CCG GGA GGA GGC GCC CCG CGG GGT CCG CAT	248
Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro His	
50 55 60 65	
GGC GGC GCG GCT TCA GGG CTG AAT GGA TGC TGC AGA TGC GGG GCC AGG	296
Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg	
70 75 80	
GGG CCG GAG AGC CGC CTG CTT GAG TTC TAC CTC GCC ATG CCT TTC GCG	344
Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala	
85 90 95	
ACA CCC ATG GAA GCA GAG CTG GCC CGC AGG AGC CTG GCC CAG GAT GCC	392
Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala	
100 105 110	
CCA CCG CTT CCC GTG CCA GGG GTG CTT CTG AAG GAG TTC ACT GTG TCC	440
Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser	
115 120 125	
GGC AAC ATA CTG ACT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG	488
Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu	
130 135 140 145	
CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG	536
Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp	
150 155 160	
ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG	584
Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly	
165 170 175	
CAG AGG CGC TAA GCCCAGCCTG GCGCCCCTTC CTAGGTCATG CCTCCTCCCC	636
Gln Arg Arg	
180	
TAGGGAATGG TCCCAGCACG AGTGGCCAGT TCATTGTGGG GGCCTGATTG TTTGTGCTG	696
GAGGAGGACG GCTTACATGT TTGTTTCTGT AGAAAATAAA ACTGAGCTAC GAAAAA	752

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Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala



65		70		75		80
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe						
	85		90			95
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp						
	100		105			110
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val						
	115		120			125
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln						
	130		135			140
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met						
	145		150			155
Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser						
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Gly Gln Arg Arg						
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Met Leu Met Ala Gln Glu Ala	
1 5	
CTG GCA TTC CTG ATG GCC CAG GGG GCA ATG CTG GCG GCC CAG GAG AGG	162
Leu Ala Phe Leu Met Ala Gln Gly Ala Met Leu Ala Ala Gln Glu Arg	
10 15 20	
CGG GTG CCA CGG GCG GCA GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG	210
Arg Val Pro Arg Ala Ala Glu Val Pro Gly Ala Gln Gly Gln Gln Gly	
25 30 35	
CCT CGG GGC CGG GAG GAG GCG CCC CGC GGG GTC CGC ATG GCG GCG CGG	258
Pro Arg Gly Arg Glu Glu Ala Pro Arg Gly Val Arg Met Ala Ala Arg	
40 45 50 55	

CTT CAG GGC TGA ATGGATGCTG CAGATGCGGG GCCAGGGGGC CGGAGAGCCG 310  
Leu Gln Gly

CCTGCTTGAG TTCTACCTCG CCATGCCTTT CGCGACACCC ATGGAAGCAG AGCTGGCCCCG 370

CAGGAGCCTG GCCCAGGATG CCCCACCGCT TCCCGTGCCA GGGGTGCTTC TGAAGGAGTT 430

CACTGTGTCC GGCAACATAC TGA CTATCCG ACTGACTGCT GCAGACCACC GCCAACTGCA 490

GCTCTCCATC AGCTCCTGTC TCCAGCAGCT TTCCCTGTTG ATGTGGATCA CGCAGTGCTT 550

TCTGCCCCGTG TTTTGTGGCTC AGCCTCCCTC AGGGCAGAGG CGCTAAGCCC AGCCTGGCGC 610

CCCTTCCTAG GTCATGCCTC CTCCCCTAGG GAATGGTCCC AGCACGAGTG GCCAGTTCAT 670

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20 25 30

Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
35 40 45

Gly Val Arg Met Ala Ala Arg Leu Gln Gly  
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Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
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<223> Beschreibung der kunstlichen Sequenz: Primer

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<223> Beschreibung der kunstlichen Sequenz: Primer

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Phe Leu Met Ala Gln Gly Ala Met Leu

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Ala Met Leu Ala Ala Gln Glu Arg Arg Val

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5

10

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Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5

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Tyr Tyr Met Asn Gly Thr Met Ser Gln Val  
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Glu Val Asp Pro Ile Gly His Leu Tyr  
1 5

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His Leu Ser Pro Asp Gln Gly Arg Phe  
1 5

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Leu Met Ala Gln Glu Ala Leu Ala Phe  
1 5

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1 5 10

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Met Ala Gln Glu Ala Leu Ala Phe Leu  
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Met Leu Met Ala Gln Glu Ala Leu Ala  
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